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 L R Y T P H P A Y A T F C R P K E N W W 63
 CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG 189
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 CAA GTC AAT AGC ATC CTT AAA GCT AAT GAA TAC AGT TTC AAA GTG CCA GAA TTT GAC GGC 309
 K N V S S I L G F D S N Q L P A N A P I 123
 AAA AAT GTC AGT TCT ATT CTT GGA TTT GAC AGC AAT CAG CTG CCT GCA AAT GCA CCC ATT 369
 E D R R S A A T C L Q T R G M L L G V F 143
 GAG GAC CGG AGA AGT GCA GCA ACC TGC TTG CAG ACC AGA GGG ATG CTT TTG GGG GTT TTT 429
 D G H A G C A C S Q A V S E R L F Y Y I 163
 GAT GGC CAT GCA GGT TGT GCT TGT TCC CAG GCA GTC AGT GAA AGA CTC TTT TAT TAT ATT 489
 A V S L L P H E T L L E I E N A V E S G 183
 GCT GTC TCT TTG TTA CCC CAT GAG ACT TTG CTA GAG ATT GAA AAT GCA GTG GAG AGC GGC 549
 R A L L P I L Q W H K H P N D Y F S K E 203
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 A S K L Y F N S L R T Y W Q E L I D L N 223
 GCA TCC AAA TTG TAC TTT AAC AGC TTG AGG ACT TAC TGG CAA GAG CTT ATA GAC CTC AAC 669
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 D N D I S L E A Q V G D P N S F L N Y L 263
 GAT AAT GAC ATC TCC TTG GAG GCG CAA GTT GGT GAT CCT AAT TCT TTT CTT AAC TAC CTG 789
 V L R V A T S G A T A C V A H V D G V D 283
 GTG CTT CGA GTG GCA TTT TCT GGA GCC ACT GCT TGT GTG GCC CAT GTG GAT GGT GTT GAC 849
 L H V A N T G D S R A M L G V Q E E D G 303
 CTT CAT GTG GCC AAT ACT GGC GAT AGC AGA GCC ATG CTG GGT GTG CAG GAA GAG GAC GGC 909

Fig. 1A

S W S A V T L S N D H N A Q N E R E L E 323
 TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA 969

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 L G L L M P F R A F G D V K F K W S I D 363
 CTT GGC TTG CTG ATG CCA TTT AGG GCA TTT GGA GAT GTA AAG TTC AAA TGG AGC ATT GAC 1089

 L Q K R V I E S G P D Q L N D N E Y T K 383
 CTT CAA AAG AGA GTG ATA GAA TCT GGC CCA GAC CAG TTG AAT GAC AAT GAA TAT ACC AAG 1149

 F I P P N Y H T P P Y L T A E P E V T Y 403
 TTT ATT CCT CCT AAT TAT CAC ACA CCT CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC 1209

 H R L R P Q D K F L V L A T D G L W E T 423
 CAC CGA TTA AGG CCA CAG GAT AAG TTT CTG GTG TTG GCT ACT GAT GGG TTG TGG GAG ACT 1269

 M H R Q D V V R I V G E Y L T G M H H Q 443
 ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA 1329

 Q P I A V G G Y K V T L G Q M H G L L T 463
 CAG CCA ATA GCT GTT GGT GGC TAC AAG GTG ACT CTG GGA CAG ATG CAT GGC CTT TTA ACA 1389

 E R R T K M S S V F E D Q N A A T H L I 483
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 R H A V G N N E F G T V D H E R L S K M 503
 CGC CAC GCT GTG GGC AAC AAC GAG TTT GGG ACT GTT GAT CAT GAG CGC CTC TCT AAA ATG 1509

 L S L P E E L A R M Y R D D I T I I V V 523
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Fig. 1B

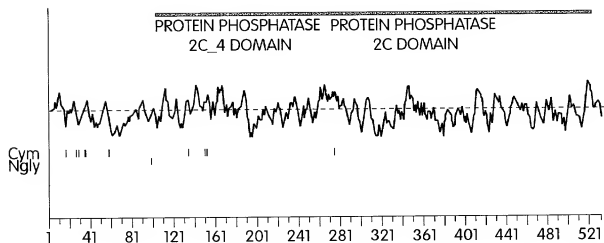


Fig. 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

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 l ++++ + r +++ +++++ ++ s++ s+ +f +++ +

26583 173 LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNLSRTYWQE 218 SEQ ID NO:2

qaakyagkhlhk.tilaerksfpegdpwEmklsdledalkesfleadtd
 + +g++ +++ + a++ f+ +d+ d + ++++ +++++

26583 219 LIDLNTGESTDIdvKEALINAFKRLDN-----DISLEAQVGDPNSFLNY 262

elrsaeasaankvltkedlssGsTavvalirgnkLyVANvGDSRavLc
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26583 263 LVLR-----VAFSGATACVAHVdGVdLHVANTGDSRAMLGvQ 299

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26583 300 EEDGSWsAVTLNDHNAQNERELERLKEHPKSEAKsvvkQDRLLGLMP 349

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26583 350 FRAFGDVKFKWSIDLQKRViesgPdQlNdnEYTKFiPPnyhtpPYLTAEp 399

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26583 400 EVT-YHRLRPQ-DKFLVLAIDGLMETMRHQDVVRIVIGEYLTGM-----H 441

meaaeklvdeaiargaeDni-*
 ++ ++ + + g ++

26583 442 HQQPIAVGGYKVILGQMHGL 461

Fig. 3A

PP2C_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98

*->es.sgknlglyrglgessmggwrkpmEDahvirp.....ffgvFD SEQ ID NO:5
 + gkn +++ g+ +s++ +++ p+ED+ ++ + ++++ + gVFd

26583 99 PEFdGKNVSSILGF-DSNQLPANAPIEDRRSAATclqtrgmLLGVFD 144 SEQ ID NO:2

GHGseaaakflskmlheilaelsfdkdeslkene.e.lk.d.ep.....
 GH+G ++++ +s++l+ ++a +l +++ ++ en+ e+++ + ++ ++

26583 145 GHAGCACSQAVSERLFYYIAVSLLPHEITLLEIENAVESGRaLLPIlqwnk 194

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26583 195 hpndyfskeasklyfnsrlrTYWqELIdlntGESTDIDVKEALINAFKRLD 244

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26583 245 NDIsleaqvcdpnsflnylvlrvaifsgATACVAHVDGVDLHVANTGDSRa 294

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26583 295 MLGVQEEEdgSW-----SAVTLSNDHNAQNERELERLKEHPKSE--AKS 336

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26583 337 VWQD-----RLGLL---LMPFRAFQDVVKFKWSIDLqKrVIEsgpdqLnd 378

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26583 423 TMHRQDVVRIVGEYLTGMHQqPIAVGGYIVTLGqMhGl1teRrtkmsv 472

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v<-*
 v

26583 523 V 523

Fig. 3B

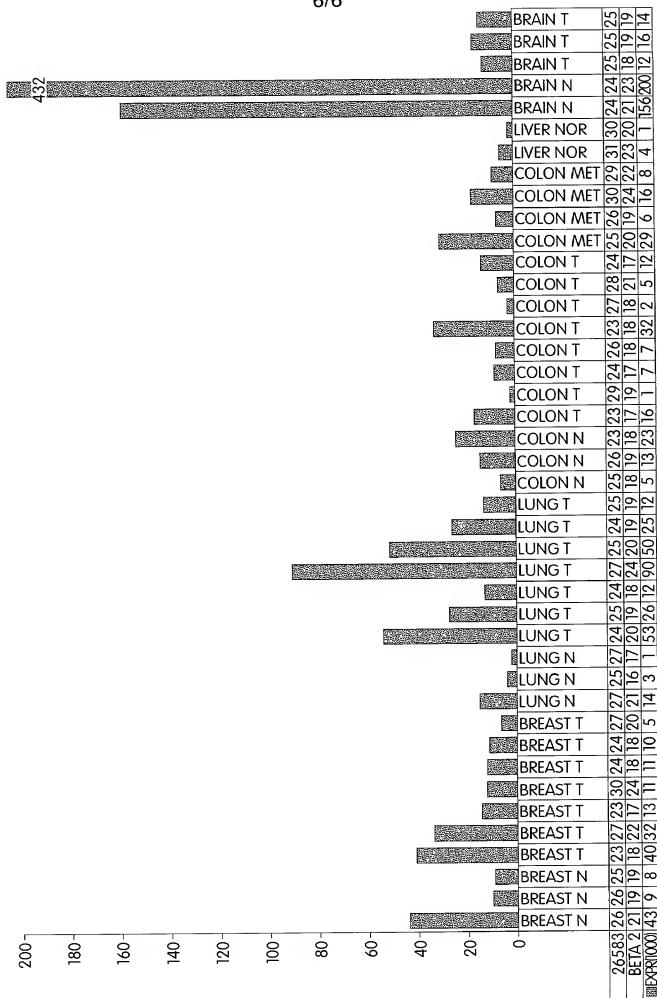


Fig. 4